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STABILIZING YIELD AND QUALITY: EARLY MATURING CHICKPEA FOR THE PRAIRIES

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Stabilizing yield and quality: early maturing chickpea for the Prairies

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A) Executive summary

Late maturity is a critical constraint to chickpea production in western Canada next to ascochyta blight. As a highly indeterminate species, chickpea continues to produce new flowers and pods over a long period of time especially during cool and wet summers. The crop is often exposed to fall frost resulting in a reduction of yield and quality. A research project was initiated to determine the potential impact of three key genetic traits: early flowering, double podding and short internode length; as part of an overall strategy to reduce the season length requirement for chickpea. Along with this, the genetics and physiological bases of earliness were studied as backup information for the ongoing chickpea breeding research.

Four crosses were made including their reciprocals as follows: double podding (272-2 X CDC Anna), early flowering (298T-9 X CDC Anna and 298T-9 X CDC Frontier) and short internode length (E100Ym X CDC Anna). CDC Anna and CDC Frontier are commercial cultivars developed for Saskatchewan while the other parents were donors of the allele(s) expressing the respective trait indicated. The F_1 was advanced to F_2 and 180 F_2 individuals from each cross were evaluated under greenhouse conditions. Next a single seed was taken from each F_2 plant and grown as an F_3 in the same greenhouse. In summer 2004, 115 of each F_3 and F_4 generations coming from individual F_2 and F_3 plants, respectively, were evaluated in microplots in the field near Saskatoon. Three lines were selected from each cross in F_4 generation and further evaluated in replicated trail in summer 2005.

In addition, intercrosses were made among genotypes carrying the key genetic traits with the aim to pyramid the genes for early flowering, double podding and short internode length and analyze their combined effect on earliness. The pedigree for this cross was 272-2/E100Ym//298T-9/E100Ym. One hundred and eighty F_2 individual plants from this cross were evaluated in the greenhouse in summer 2004. During summer 2005 an F_3 generation from this population was evaluated in the field at Preston, Saskatoon. Data were collected on days to flowering, days to first podding, days to first pod maturity, percent pod maturity at four months after planting, and other agronomic traits for all the single and double cross populations.

The populations from single crosses displayed wide ranges of variability in days to first pod maturity and percent pod maturity at four months after planting. Some lines that were earlier than the best parents and presumably superior to available cultivars in terms of earliness have been identified. These were mostly from the double podding cross. Mean percent pod maturity at four months after planting was higher for the double podded genotypes over their single podded counterparts, especially in the field grown replicated

experiment. The double podded lines on average matured about ten days earlier than the parents and other check varieties. Increase in height between flowering and maturity stages was relatively low for the double podded genotypes. Double podding likely increases sink size, delimits post-flowering vegetative growth, and thereby leads to a more uniform maturity of pods.

The early flowering trait had effects on days to first podding and days to maturity of these lower pods. Time to flowering was linearly and positively associated with these earliness traits and 32% of the variation in days to first pod maturity was controlled by days to flowering. It appears that incorporation of early flowering genes advanced the beginning of maturity of lower pods, which enabled plants to progress well in maturity before the occurrence of frost.

We hypothesized that short internode length may reduce the time for the development of sequential nodes and overall crop growth duration. The population from this cross segregated into 3 normal: 1 dwarf genotypes. However, all the short internode genotypes were late to flower, pod and mature. Shortening the internode length may still be beneficial for early crop maturity, but the allele from our short internode parent had unfavorable effects on overall crop growth and development.

For the gene pyramiding population, days to first pod maturity ranged from 57 - 80 days with some genotypes earlier than the best parent 272-2 by up to one week. The variability in percent pod maturity at four months after planting was correspondingly high, ranging from 46-100%. A few genotypes had over 90% pod maturity at this time, meaning they had reached full maturity in four months. However, the same level of earliness may not be attained under field condition, especially in wet seasons. The identified early genotypes were superior to 272-2 and CDC Anna, which had mean percent pod maturity of 84% and 74%, respectively.

Studies on the genetic control of earliness traits revealed that the variation in days to flowering is best explained by two major genes and polygenes. Broad sense heritability estimates were greater than 80% across populations. However, there appeared to exist epistatic interaction between the two major genes, indicating that selection for early flowering would be more effective if delayed to later generations. Days to first pod maturity and percent pod maturity had moderate heritability estimates. The predicted genetic advance was high (38% of the population mean) for days to first pod maturity. This shows that significant improvement can be made in these traits through selection.

The patterns of dry matter accumulation and partitioning as related to earliness were also studied using the five crossing parents 272-2, 298T-9, E100Ym, CDC Anna and CDC Frontier over two years (2003 and 2004). Based on maturity ranking, 272-2 was the earliest, while E100Ym was the latest to mature. The genotypes studied had generally similar patterns of dry matter accumulation, but were different in partitioning efficiency to different plant parts. Genotype 272-2 was superior in partitioning of dry matter to pods early in the season. The proportion of dry matter in the pods (seed + pod wall) was about 72% of the total biomass at the stage of maximum dry matter accumulation in 272-2,

while it was only 22% for the late maturing genotype E100Ym. This probably shows that as part of the strategy for early crop maturity in chickpea, preferential partitioning of dry matter to pods has terminated growth early in 272-2.

B) Technical Report

Background

Chickpea (*Cicer arietinum* L.) is known for its multiple benefits including food and feed uses, wide export market potential, and soil-amelioration purposes. Thus, it is an ideal species for crop diversification in western Canada. Other rotational benefits of chickpea including opportunities to break pest (diseases, insects and weeds) cycles of non-leguminous crops and nutrient recycling due to its deep root system. Because of its drought tolerance chickpea may also be suitable for marginal lands. The global demand for chickpea is rising, indicating its prospective future.

The chickpea crop is well adapted to the Mediterranean and to the cool season in the semi-arid tropics (Jettner et al. 1999). This crop was recently introduced to western Canada and faces unique challenges. It is the only production region in the world where chickpea matures under conditions of declining temperature. This coupled with end-of-season precipitation in some years triggers the indeterminate nature of the crop and delays maturity. In this environment, the chickpea crop is often exposed to frost damage resulting in reduced yield and quality.

Early maturity has been a key objective in the University of Saskatchewan, Crop Development Centre chickpea breeding program since its inception in the early 1990's. Since that time, many accessions and breeding lines were screened for earliness. Differences were detected and some earlier cultivars have been released, but none was found to possess the desired level of earliness for this environment.

Major improvements in crop plants have been achieved through changes in important morpho-physiological traits such as reduced height, increased harvest index, increased ratio of reproductive to vegetative period, improved partitioning of assimilates to seeds and increased remobilization of assimilates to storage organs. The underlying principle is that changes in those traits resulted in a more efficient plant system in terms of producing grain or economic yield within a growing season. Likewise, it seems necessary to employ similar strategies for inducing earliness in chickpea, where existing variation for this trait is not high enough to make substantial changes.

Double podding, early flowering and short internode length are among the key genetic traits related to developmental characteristics in chickpea and may have an effect on maturity. When combined, the interactive effect of all these traits could bring the desired level of earliness, resulting in a low risk crop for the prairies. In prairie agriculture, early maturity means yield stability in most years because with early maturity, a crop can finish producing yield before frost ends the growing season. For the project under report, the above mentioned three key genetic traits were investigated as an alternative strategy to induce earliness in chickpea in its new western Canadian environment.

Double podding: Sheldrake et al. (1978) reported that the double-podding character could confer 6 to 11% yield advantage under conditions in which the character is well-expressed. The allele for double pods also had a positive effect on the stability of seed yield over locations and years (Rubio et al. 1998). The contribution of double podding trait to yield stability might have stemmed from its involvement in early maturity. Increase in number of pods per reproductive node and subsequent higher total pod set may increase demand for photoassimilates resulting in an earlier transition to physiological maturity.

Early flowering: Quantification of the flowering response of a number of chickpea genotypes has indicated that a wide range of flowering times exist in chickpea (Singh et al. 1983). The flowering genes seemingly influence maturity type through their effects on the onset of the reproductive stage. Early flowering lines may mature early with little or no effect on the reproductive period of the crop. This may also prolong the reproductive period, which is a major yield determinant in chickpea (Bonfil and Pinthus, 1995). If extra-early flowering genotypes became available for environments where the growth duration is delimited as a consequence of end-of-season drought, high temperature or frost, chickpea productivity may increase and stabilize at a higher level.

Short internode length: In chickpea, a phenotypically distinct dwarf type E100Ym with short internode length was identified at ICRISAT. The hypothetical advantage of utilization of short internode length in chickpea breeding is to increase the proportion of assimilates partitioned into grain. Dahiya et al. (1990) reported that medium height chickpea recombinants from a cross between E100Ym and conventional types showed better performance compared to the parents for total number of pods per plant and seed yield. An additional merit is that the time required to enlarge or produce more internode cells is saved and hypothetically the plants mature earlier.

Success in plant breeding in part depends on understanding of the genetic control and physiological basis of commercially important traits. Along with the primary target of inducing earliness through secondary traits (double podding, early flowering and short internode length), the genetics and physiological bases of earliness in chickpea were studied. This information could be utilized to design effective selection methods to bring substantial improvement in chickpea with respect to earliness and yield. Taken together the project had three major objectives:

1. To determine whether the timing of crop maturity is related to dry matter accumulation and partitioning.

2. To estimate genetic variability, heritability and genetic gain for earliness traits.

3. To test whether that the key genetic traits early flowering, double podding and short internode length induce earliness individually or when combined (i.e. gene pyramiding).

THEME I: Relationships of timing of crop maturity with post-flowering dry matter accumulation and partitioning in chickpea

The main chickpea breeding challenge in western Canada is to enable seed maturation to occur before first frost while maximizing yield within the short growing season. This could be attained through faster rate of crop growth and/or efficient partitioning of dry matter to the grain. The present work was aimed at determining the patterns of dry matter accumulation and partitioning in early vs. late maturing chickpea genotypes such that the strategy of growth for earlier crop maturity would be elucidated.

Materials and Methods

Field experiments were conducted at Goodale in 2003 and at Goodale, Preston and Swift Current in 2004. Goodale and Preston are near Saskatoon (52.1°N, 106.4°W), while Swift Current is at 50.6°N, 107.4°W. Five diverse genotypes including CDC Frontier, CDC Anna, 272-2, 298T-9, and E100Ym were used for this investigation. These were arranged in randomized complete block design with four replications. Each genotype was planted in four row plots with 4 m row length. Spacing was 6.5 cm between plants and 30 cm between rows, resulting in a target population density of 44 plants /m^2 as recommended for western Canada.

Beginning two months after planting and every fifteen days following, plant samples consisting of 0.3 m^2 area (0.5 m X 0.6 m) were taken from the two central rows of each plot. The plant samples were separated into fractions of leaf, stem, and pod. Pod consisted of pod walls and seeds. The samples were dried at 81°C for 72 hours and then dry weights were determined. Plant height (cm) was determined from five randomly selected plants. Days to flowering and days to maturity were recorded on the remaining plants in each plot. Grain yield (kg/ha) and 100 seed weight (g) were also recorded after threshing and cleaning the seeds.

Analysis of variance (ANOVA) was carried out on days to flowering and maturity, plant height, grain yield and 100 seed weight using SAS statistical packages (SAS Institute Inc., 1999). A split-plot in time analysis was carried out for amount of dry matter accumulation in different plant tissues stem, leaf, pod, vegetative (leaf + stem), and total (leaf + stem + pod) using SAS PROC MIXED with a REPEATED statement for the sampling dates (Bowley, 1999; Littell et al. 1998). A combined ANOVA was performed for data collected at three locations (Preston, Goodale and Swift Current) in 2004. Partitioning coefficient was estimated by the gradient of the regression of pod dry weight on total dry weight over sampling dates (Ellis et al. 2000).

Results and Discussion

Crop phenology: Seasonal rainfall and cumulative mean air temperature were variable across the site-years. Generally, 2004 was cool and wet, while 2003 was dry. The variation in climatic conditions was heavily reflected in crop phenology. The genotypes flowered in 37-46 days and matured in 93-107 days at Goodale in 2003 (Table 1.1). Crop growth was slow in 2004 and flowering was delayed by about two weeks and maturity by more than five weeks during this season as compared to 2003. Kamali and Royd (2000)

pointed out that crops respond to conditions of favorable growth by delaying the timing of phenological events or, alternatively, by advancing the timing of events when conditions of stress are imposed.

The difference among genotypes in days to flowering and maturity was significant ($p \leq 0.05$) across all site-years (Table 1.1). Genotype 272-2 was consistently the earliest to flower and mature. CDC Frontier was the latest genotype to flower, but matured at the same time as 298T-9, though the latter preceded CDC Frontier by about one week in days to flowering.

Table 1.1. Days from planting to 50% flowering and to physiological maturity in five chickpea genotypes across different site-years

Genotype	50% flowering				Physiological maturity*		
	Goodale 2003	Goodale 2004	Preston 2004	SC 2004	Goodale 2003	SC 2004	Preston 2004
272-2	37	47	50	54	93	129	128
298T-9	38	46	52	55	97	135	139
E100Ym	42	49	53	56	107	146	Late**
CDC Anna	44	53	56	58	97	139	Late**
CDC Frontier	46	54	59	59	100	135	142
Mean	42	50	54	56	99	135	-
LSD $_{(0.05)}$	0.9	1.1	0.8	1.0	2.6	5.0	-
CV (%)	1.3	1.4	1.0	0.9	1.7	2.0	-

- SC – Swift Current, * - All genotypes were affected by frost before physiological maturity at Goodale 2004, thus data are not reported, ** - Affected by frost before physiological maturity

Seed yield: As expected, the released cultivars CDC Frontier and CDC Anna were superior in grain yield at both Goodale 2003 and Swift Current 2004 (Table 1.2). However, when assessed on fully matured seeds (excluding green, shriveled, immature seeds), grain yield of 272-2 exceeded the late maturing genotypes including CDC Anna during the unfavorable 2004 season. Genotype 272-2 had about 92% mature seed as a proportion of the total grain yield, whereas the late genotypes CDC Anna and E100Ym had less than 40% mature seed (Table 1.2). The early maturing genotype 272-2 also had relatively more stable yield over the two seasons. It is apparent from this study that correct timing of maturity is not only important for adaptation, but also will have substantial benefits in terms of increasing yield and quality of chickpea in the Prairies. At Goodale 2004 and Preston 2004 the crop was affected by frost, thus yield data were not obtained.

Patterns of dry matter production: Analysis of variance revealed significant differences among genotypes and sampling dates in amounts of total (stem, leaf and pod), vegetative (stem and leaf) and pod dry weights. For the genotypes studied, total dry matter showed a continuously increasing trend over sampling dates in both years, though the increase was at a decreasing rate beginning in mid-season (Fig.1.1). The released varieties (CDC Frontier and CDC Anna) had high dry matter accumulation across

sampling dates and reached greater maximum dry matter content than the other genotypes. However, distinctive patterns of total dry matter accumulation were not detected which corresponded with the differences in maturity duration of genotypes.

Table 1.2. Seed yield, 100 seed weight, and plant height of five chickpea genotypes evaluated at Goodale in 2003 and Swift Current (SC) in 2004

Genotype	Seed yield (kg/ha)		100 seed weight (g)		Plant height (cm)	
	Goodale 2003	SC 2004	Goodale 2003	SC 2004	Goodale 2003	SC 2004
272-2	2271	2199 (2051)	11.2	13.7	27.0	45.3
298T-9	2004	2217 (1547)	16.6	20.3	33.2	50.0
E100Ym	1492	1610 (650)	29.9	37.0	24.2	43.0
CDC Anna	2333	3278 (1216)	19.0	24.0	39.0	57.7
CDC Frontier	3479	4913 (2094)	30.6	37.3	39.0	59.0
Mean	2316	2843 (1512)	21.4	26.5	32.5	51.0
CV (%)	11.8	15.7 (12.3)	4.4	3.1	8.5	3.2
$LSD_{(0.05)}$	429	856 (507)	1.5	1.6	4.3	3.1

Figures in parenthesis are the yield as measured for normal, fully matured seeds.

Fig. 1.2 shows the trend in vegetative (stem and leaf) dry weight across sampling dates in the five genotypes tested. In both 2003 and 2004, the vegetative dry matter started to decline earlier in the early maturing genotype 272-2, as compared to others, and was significantly lower in this genotype at the last sampling date. Vegetative dry matter started to decline two weeks later for the late maturing genotypes viz. E100Ym, CDC Anna and 298T-9 in 2003, or kept increasing throughout the sampling period in 2004. CDC Frontier, which was latest to flower but was intermediate in maturity ranking, had similar trend as 272-2, however, the amount of vegetative dry matter at each sampling date was high for CDC Frontier. Pedersen and Lauer (2004) also observed significant differences among soybean genotypes in dry matter partitioned into stems and leaves during later reproductive stages, from R5 stage onwards. This suggests that early cessation of post-flowering vegetative growth, and thereby the tendency toward a more determinate growth habit would contribute to timely maturity in chickpea in a Canadian Prairie environment.

The decline in vegetative dry matter during the reproductive stage is probably due to nutrient remobilization to reproductive organs and leaf senescence. In soybean, the decline in dry matter accumulation was consistent with the onset of leaf senescence and coincided with the decline in leaf area index (Pedersen and Lauer 2004). However, insufficient dry matter production (i.e., source) may be a major limiting factor to high seed yield in cases where post-flowering vegetative growth is limited. These genotypes depend on dry matter at or before flowering to achieve high total dry matter. Pre-flowering vigorous growth may help to optimize total dry matter accumulation in this case. Differences exist in growth vigor in chickpea germplasm and selection for faster growth rate during the vegetative phase would improve dry matter accumulation and leaf area index early in the season (Sabaghpour et al. 2003).

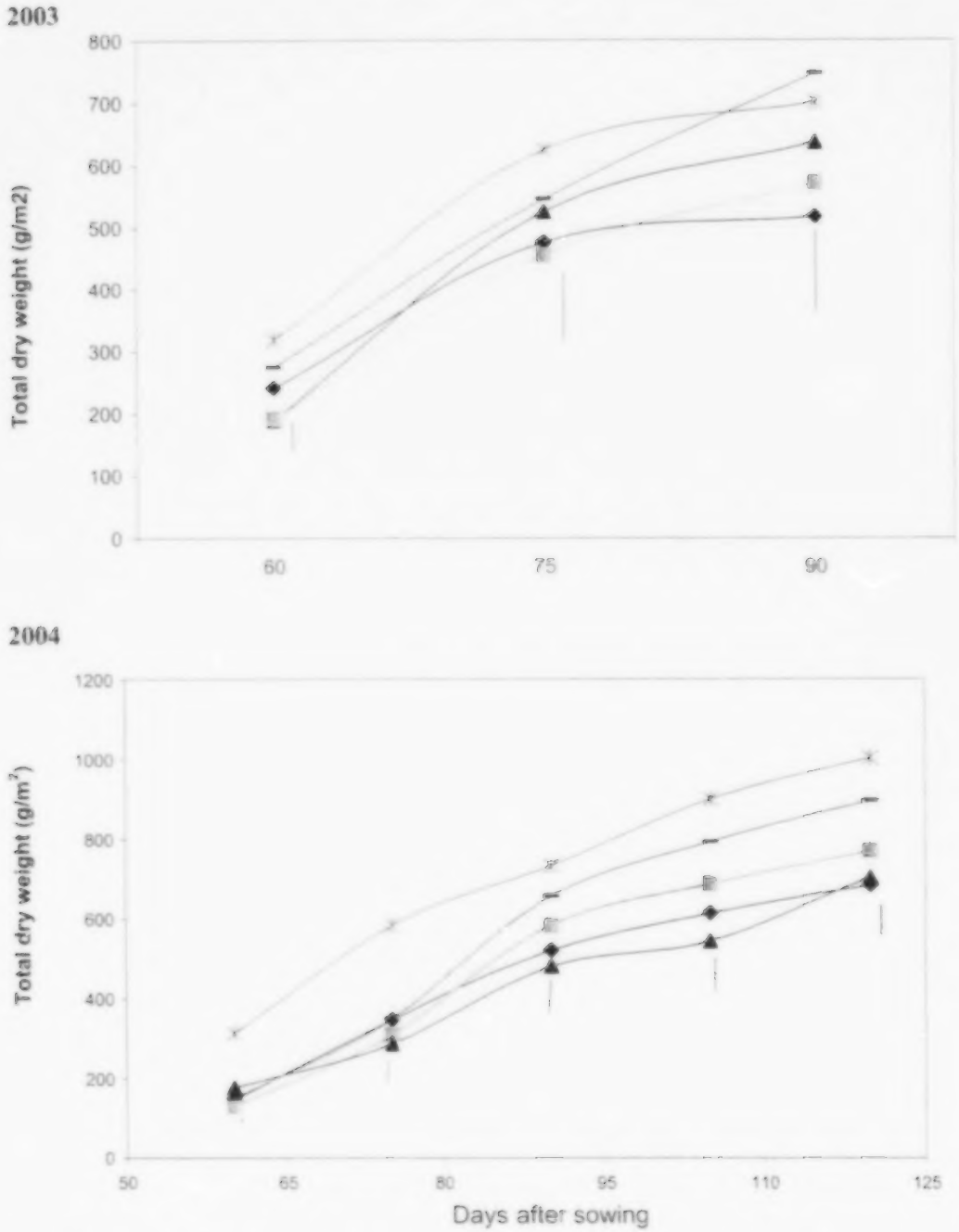


Fig. 1.1. Total dry matter accumulation at different sampling dates in five chickpea genotypes (◆ 272-2, ■ 298T-9, ▲ E100Ym, – CDC Anna, * CDC Frontier) assessed at Goodale in 2003 and Goodale, Preston and Swift Current in 2004. Data from 2004 is the mean of the three locations. Vertical bars show LSD at P = 0.05.

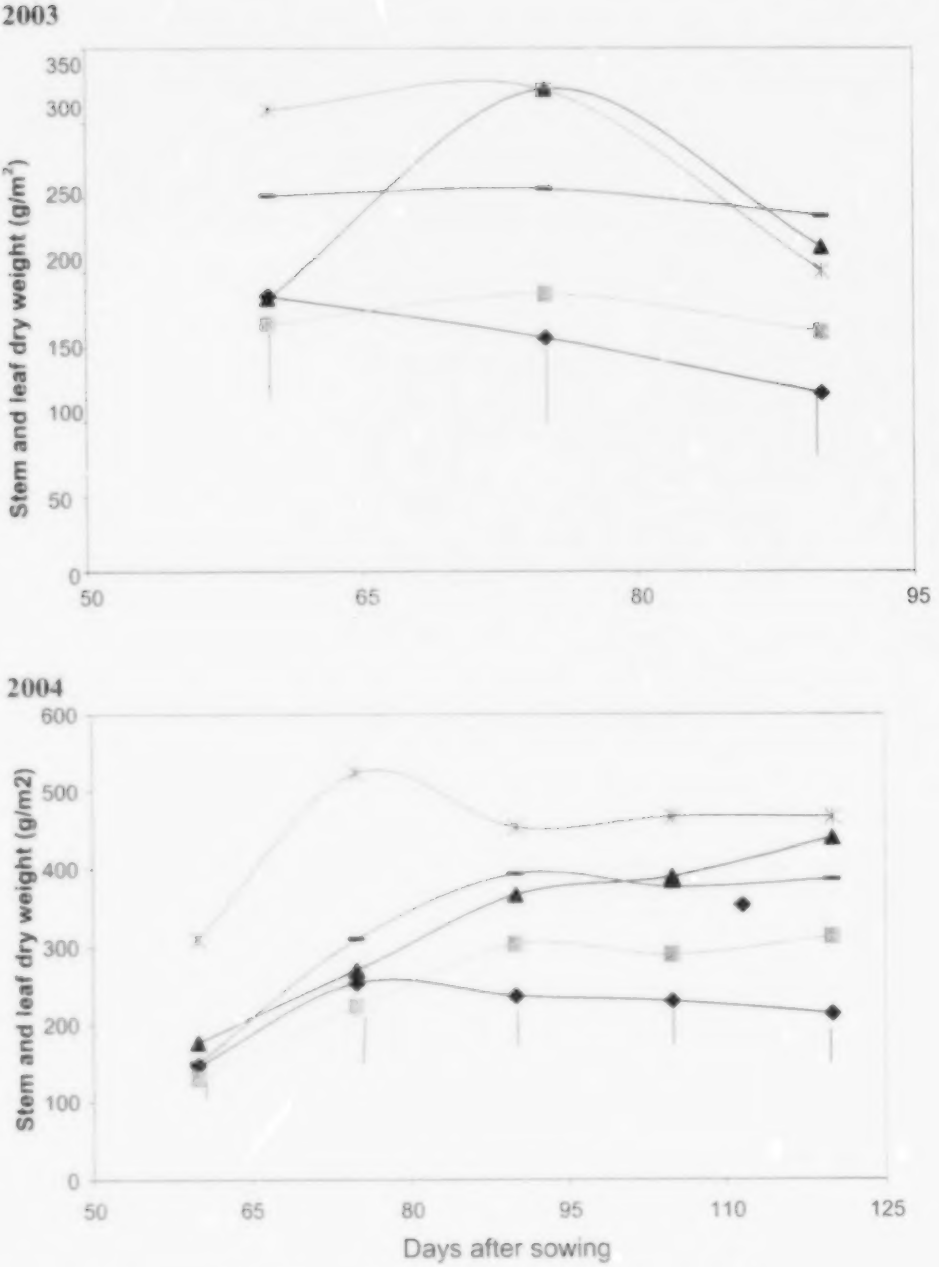


Fig. 1.2. Stem and leaf dry weights at different sampling dates in five chickpea genotypes (● 272-2, ■ 298T-9, ▲ E100Ym, – CDC Anna, * CDC Frontier) assessed at Goodale in 2003 and Goodale, Preston and Swift Current in 2004. Data from 2004 is the mean of the three locations. Vertical bars show LSD at P = 0.05.

Partitioning of dry matter: The increase in pod dry weight over sampling dates followed a linear trend in the genotypes studied (Fig. 1.3). The same pattern was also observed for two soybean cultivars in seed and pod wall dry weight (Beaver and Cooper, 1982). Early flowering genotypes 272-2 and 298T-9 had significantly higher pod dry weight initially, i.e. at the first sampling date in 2003 and at the second sampling date in 2004. However, these were surpassed by improved cultivars (CDC Frontier and CDC Anna) in the subsequent sampling dates.

Partitioning coefficient, as determined by the slope of the regression of pod dry weight on total dry matter, varied among genotypes (Table 1.3). After the first sampling in 2003 and second sampling in 2004, 272-2 and CDC Frontier had greater rate of pod dry weight accumulation than the rate of vegetative dry weight. Consequently 272-2 and CDC Frontier had high partitioning coefficients of about 1.0 or more at most site-years (Table 1.3). Due to delayed planting and long maturity duration at Goodale 2004, partitioning coefficient values were low for all genotypes at this site-year. Seed growth can be greater than the concurrent rate of total dry matter accumulation, i.e., partitioning coefficient values exceeding 1.0, since C and N would be mobilized from vegetative tissue for use by seeds (Boote and Tollenaar 1994). This probably enabled the late flowering genotype CDC Frontier to mature simultaneously with the early flowering genotype 298T-9 (Table 1.1). In cotton, another indeterminate species, an early maturing cultivar partitioned a greater proportion of dry matter into reproductive organs than did a late-maturing cultivar and the former had significantly higher final harvest index (Pace et al. 1999). Higher partitioning coefficient apparently leads to higher harvest index. More efficient partitioning to grain and consequently improved harvest index is therefore a factor related to early crop maturity in chickpea.

Table 1.3. Estimates of partitioning coefficient for five chickpea genotypes grown at four site-years

Genotype	Preston 2004	Swift Current 2004	Goodale 2003	Goodale 2004
272-2	1.04 (0.11)	1.00 (0.02)	1.20 (0.10)	0.61 (0.09)
298T-9	0.84 (0.06)	0.88 (0.08)	0.99 (0.07)	0.52 (0.07)
E100Ym	0.43 (0.08)	0.68 (0.12)	0.78 (0.28)	0.43 (0.06)
CDC Anna	0.80 (0.10)	0.84 (0.17)	1.02 (0.03)	-
CDC Frontier	1.00 (0.21)	0.98 (0.08)	1.19 (0.27)	0.51 (0.12)

- observation missing;
values in parentheses are standard error.

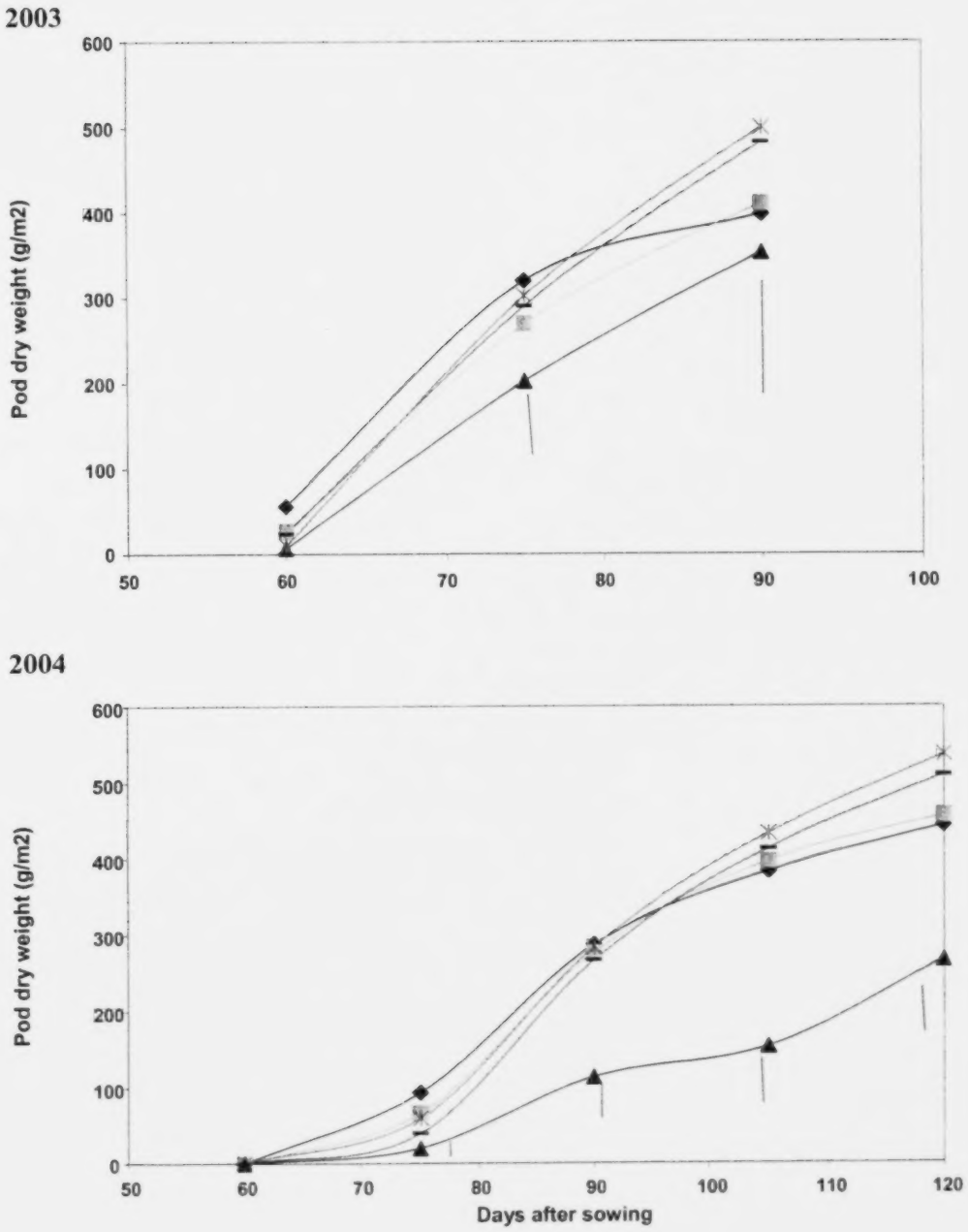


Fig. 1.3. Pod dry weights at different sampling dates in five chickpea genotypes

(◆272-2, ■ 298T-9, ▲ E100Ym, – CDC Anna, * CDC Frontier) assessed at Goodale in 2003 and Goodale, Preston and Swift Current in 2004. Data from 2004 is the mean of the three locations. Vertical bars show LSD at P = 0.05.

THEME 2: Genetic analysis of earliness in chickpea

Earliness is the end result of different developmental components, which are interrelated and which presumably can be manipulated separately in the breeding process. At least three major developmental stages related to earliness are recognized in chickpea. These are the time taken to beginning of reproductive growth (days to flowering), the time to beginning of maturity of lower pods (days to first pod maturity), and the proportion of matured pods at the end of the growing season (percent pod maturity). Effective alteration of maturity can best be achieved by selecting for more than one component of earliness. The objective of this study was to determine the genetic control of three major earliness traits in chickpea: days to flowering, days to first pod maturity, and percent pod maturity at four months after planting.

2.1. Days to flowering

Experimental procedure: Three crosses were made between moderately early (272-2 and 298T-9) and late (CDC Anna and CDC Frontier) flowering genotypes. 272-2 was crossed to CDC Anna, while 298T-9 was crossed to both late parents. The F_1 was advanced to F_2 and 180 F_2 plants were evaluated from each cross under greenhouse conditions in summer 2003. A single seed was taken from each F_2 plant and grown as F_3 in the same greenhouse during fall/winter. In both cases one plant was grown in each 20 cm diameter pot filled with Redi-Earth potting soil (W.R. Grace and Co., Canada). The two parental genotypes were included as repeated checks. During summer 2004 all the P_1, F_1, P_2, F_2, and $F_{2:3}$ populations were evaluated in field experiment near Saskatoon. Data was recorded on days to flowering and other earliness traits such as days to first pod maturity and percent pod maturity.

Data analysis: The distribution of time to flowering for F_2 populations from the greenhouse experiment was tested for normality using SAS PROC UNIVARIATE NORMAL (SAS Institute, Cary, NC). The C scaling test of Mather and Jinks (1982) was used to determine whether that the additive-dominance model is sufficient to explain the variation in time to flowering, or whether the difference between observed and expected generation means is significant as could occur with epistasis. It was determined from the generation means of the experiment conducted under field condition as:

$$4F_2 - P_1 - 2F_1 - P_2 = C,$$

C should equal zero, apart from standard error.

Joint segregation analysis (JSA) of multiple generations P_1, F_1, P_2, F_2, and $F_{2:3}$ was used to determine the genetics of early flowering in chickpea. This method has newly been developed for analysis of major gene-polygenes mixed quantitative variation in plants (Wang and Gai, 2001). The steps used were as follows. First, some possible genetic models were hypothesized and likelihood functions were established for the different genetic models. Twenty six genetic models belonging to five model classes were tested to select the one that best explained the variation in time to flowering in chickpea (Table 2.1). Second, maximum likelihood estimates of the parameters contained in each genetic model were obtained. Finally, the best fitting genetic model was selected based on Akaike's Information Criterion (AIC) (Akakie, 1997 cf Knott *et al.*, 1991).

Table 2.1. Genetic models in the joint segregation analysis of the five generations of P_1, F_1, P_2, F_2 and $F_{2:3}$

Class	Major gene	Polygenes	Model type	
			Only major Gene	Mixed major gene & polygenes
Polygenes	-	Additive-dominant [a][d]	-	C-1
	-	Additive-dominant-epistasis [a][d][i][j][l]	-	C-2
One major gene	Additive-dominant a, d	Additive-dominant-epistasis [a][d][i][j][l]	A-1	D
	Additive-dominant a, d	Additive-dominant [a][d]	A-1	D-1
	Additive a (d=0)	Additive-dominant [d][h]	A-2	D-2
	Completely dominant d(d=a)	Additive-dominant [d][h]	A-3	D-3
	Completely negative dominant d (-d=a)	Additive-dominant [d][h]	A-4	D-4
Two major genes	Additive-dominant-epistasis $a_1, a_2, d_1, d_2, I, j_{12}, j_{21}, l$	Additive-dominant-epistasis [a][d][i][j][l]	B-1	E
	Additive-dominant-epistasis $a_1, a_2, d_1, d_2, I, j_{12}, j_{21}, l$	Additive-dominant [a][d]	B-1	E-1
	Additive-dominant $a_1, a_2, a_1, a_2, I = j_{12} = j_{21} = l = 0$	Additive-dominant [a][d]	B-2	E-2
	Additive $a_1, a_2 d_1 = d_2 = 0$	Additive-dominant [a][d]	B-3	E-3
	Equally additive $a (=a_1 = a_2, d_1 = d_2 = 0)$,	Additive-dominant [a][d]	B-4	E-4
	Completely dominant $(a_1 = d_1, a_2 = d_2)$	Additive-dominant [a][d]	B-5	E-5
	Equally dominant $a = a_1 = d_1 = a_2 = d_2$	Additive-dominant [a][d]	B-6	E-6

a, d - additive and dominance effects of major gene for model A and D; a_1, d_1 - additive and dominance effects of the first major gene for model B and E; a_2, d_2 – additive and dominance effects of the second major gene for model B and E; i, j_{12}, j_{21}, and l – additive x additive, additive x dominance, dominance x additive, dominance x dominance epistatic effects between the two major genes; [d],[h],[i][j][l] – additive effects, dominance effects, additive x dominance (or dominance x additive) and dominance x dominance epistatic effects of the polygenes.

Results and discussion: The F_2 populations evaluated in the greenhouse showed continuous variation for time to flowering in all three crosses. The majority of the individuals fell between the two parents, but a few were up to two days earlier than the early parent and others were a few days later than the respective late parent. However, the distribution of the F_2 population for time to flowering deviated from normal distribution (Table 2.2). This deviation is probably an indication of the involvement of major gene(s) in the inheritance of time to flowering in chickpea.

Summer 2004 was cooler than average at Saskatoon. As a result crop growth was very slow and flowering was delayed. Under these conditions the early parents flowered in 53-54 days from planting, whereas the late parents took 61-63 days (Table 2.3). The classical C scaling test revealed the involvement of epistatic gene action in the genetic control of time to flowering in chickpea. In all three crosses the difference between generations' means was significantly higher than that could be explained by the additive-dominance genetic model (Table 2.3). Previously, Girase and Deshmukh (2000) reported duplicate gene action for time to flowering in chickpea. Kidambi *et al.* (1990) also noticed digenic

interaction for this trait. With the presence of epistatic gene action for time to flowering, it follows that selection would be more effective if delayed to later generations.

Table 2.2. Minimum, mean and maximum number of days to flowering and test for normal distribution of this trait in three F_2 populations of chickpea grown under greenhouse conditions

Population	Days to flowering			Distribution (Shapiro-Wilk test)	
	minimum	mean	maximum	Statistic	Pr < W
272-2 x CDC Anna	20	24.5	28	0.95	0.00
298T-9 x CDC Anna	19	23.5	28	0.97	0.00
298T-9 x CDC Frontier	19	24.0	29	0.97	0.03

Pr < W < 0.05 shows significant deviation from normal distribution

Table 2.3. C scaling test for days to flowering in three chickpea crosses assessed in the field at Saskatoon in 2004

Generation	Mean ± SE		
	272-2 X CDC Anna	298T-9 X CDC Anna	298T-9 X CDC Frontier
P_1	61 ± 0.3	61 ± 0.3	63 ± 0.4
P_2	54 ± 0.3	54 ± 0.2	53 ± 0.2
F_1	61 ± 0.5	61 ± 0.3	61 ± 0.4
F_2	56 ± 0.2	57 ± 0.2	57 ± 0.3
C	-12.4 ± 1.2***	-7.5 ± 1.3***	-9.3 ± 1.6***

***-significant at P < 0.001, SE – standard error, P_1 and P_2 – late and early parent, respectively

The joint segregation analysis revealed that the variation in time to flowering in chickpea was best explained by mixed two major genes and polygenes model (Table 2.4). Model E-1 had lowest AIC for the 272-2 X CDC Anna and 298T-9 X CDC Anna populations, whereas model E-2 did for 298T-9 X CDC Frontier population. The difference is that with E-1 there is interaction between the two major genes, but E-2 shows only additive-dominant type of gene action. However, it is indicated above that the C scaling test revealed the presence of epistasis in all three populations. The difference between JSA and C scaling test for the third cross could be attributed to the F_3 population structure as data for this generation was used in the JSA but not in the C scaling test.

A high level of phenotypic variation occurred for time to flowering within each population and in both F_2 and $F_{2:3}$ generations under field conditions (Table 2.5). The majority of the variation in time to flowering was accounted for by the two major genes. Polygenes controlled 0-21% of the phenotypic variation depending upon cross and generation, and should be the basis for earlier and later transgressive segregants observed. Heritability of major genes was very high, above 90% in some crosses and generations. For both major genes (a_1 and a_2) the late flowering alleles showed complete dominance as depicted by negative values greater than one (Table 2.5). The present study also showed that the digenic interaction between the two major genes was mainly additive x additive type. This is generally fixable and can be exploited with later generation selection.

Table 2.4. Akakie's Information Criteria (AIC) values under various genetic models for time to flowering in three chickpea crosses

Model*	Population			Model*	Population		
	I	II	III		I	II	III
A-1	1277.0	1396.7	1340.5	D	1198.9	1304.6	1240.6
A-2	1289.7	1392.7	1391.9	D-1	1215.8	1325.7	1259.4
A-3	1371.8	1439.8	1455.6	D-2	1229.8	1339.6	1276.6
A-4	1323.3	1449.5	1394.6	D-3	1222.5	1337.7	1319.6
B-1	1196.4	1331.3	1306.6	D-4	1213.8	1332.3	1257.8
B-2	1216.4	1298.4	1248.1	E	1197.5	1283.3	1211.1
B-3	1218.1	1357.1	1340.0	E-1	1193.8	1282.1	1221.5
B-4	-	-	-	E-2	1246.4	1341.0	1199.2
B-5	1339.6	1406.7	1433.3	E-3	1258.8	1304.2	1304.7
B-6	-	-	-	E-4	1281.5	1406.1	1323.4
C	1234.9	1345.4	1281.6	E-5	1219.4	1334.8	1215.9
C-1	1281.9	1406.8	1323.7	E-6	1281.8	1406.8	1323.7

* - complete description given in Table 2, dash indicates that the model did not converge
I - 272-2 X CDC Anna, II - 298T-9 X CDC Anna, III - 298T-9 X CDC Frontier
Lowest AIC values in each cross underlined, so are the best fitting model

Table 2.5. Estimates of genetic parameters of days to flowering in three chickpea crosses, where I - 272-2 X CDC Anna, II - 298T-9 X CDC Anna, III - 298T-9 X CDC Frontier

1st order parameter	Estimates			2nd order parameter	Estimates in F_2			Estimates in $F_{2:3}$		
	I	II	III		I	II	III	I	II	III
M	54.64	54.0	57.7	σ^2_p	4.66	8.46	10.6	4.19	5.84	9.6
a_1	0.63	1.24	4.18	σ^2_{mg}	3.03	7.68	9.6	3.16	5.69	8.2
a_2	0.60	-0.24	2.15	σ^2_{pg}	0.00	0.03	0.0	0.87	0.07	1.3
d_1	-1.75	-3.77	-6.72	σ^2_e	1.63	0.76	1.0	0.16	0.08	0.1
d_2	-1.78	-1.33	-2.16	H^2_{mg} (%)	65.0	90.7	90.4	75.4	97.5	85.6
I	2.50	3.10	-	H^2_{pg} (%)	0.00	0.35	0.0	20.7	1.21	13.3
j_{12}	0.16	-0.25	-							
j_{21}	0.11	1.01	-							
L	0.08	-1.54	-							
[a]	2.61	2.87	-1.75							
[d]	5.60	13.2	12.5							

m- population mean, a_1- additive effect of major gene 1, a_2- additive effect of major gene 2, d_1- dominance effect of major gene 1, d_2- dominance effect of major gene 2, i- additive x additive epistasis, j_{12}- additive x dominance interaction, j_{21}- dominance x additive interaction, l- dominance x dominance epistasis, [a]– additive effect of polygenes, [d]- dominance effect of polygenes, σ^2– variance, p – phenotype, mg– major gene, pg- polygenes, e- environment, H^2- heritability in broad sense

2.2. Days to first pod maturity (DFPM) and percent pod maturity (PPM)

Population: The plant population used for this study was from the same crosses as for the inheritance of time to flowering (see section 2.1). In addition to what has been described in that section, F_3 and F_4 generations were evaluated simultaneously in the field during the 2004 summer season. Thirty plants were grown in each microplot (0.6 m x 1 m). One hundred and fifteen genotypes were evaluated along with replicated check entries for each F_3 and F_4 generations for each cross. These were arranged in an augmented randomized complete block design. Data were collected on DFPM and PPM at four months after planting.

Data analysis: The analysis was carried out using SAS PROC GLM following the method given by Scott and Milliken (1993). Genetic variability for DFPM and PPM was computed for data from the F_4 generation. Environmental variance was determined from the variability for homozygous parental genotypes used as repeated checks. Thereafter the following genetic parameters were determined.

- Narrow sense heritability (h^2):- calculated from parent-offspring (F_3-F_4) regression following the method of Smith and Kinman (1965).

  $$h^2 = b/2r_{xy} = 4/7\ (b) \text{ for } (F_4, F_3)$$

  where b is the regression coefficient and r_{xy} is the probability that a random gene at a specific locus in $X(F_4)$ is identical by descent to a random gene at the same locus in $Y(F_3)$.

- Predicted genetic gain (GA):- determined as the product of heritability and selection differential with 10% selection intensity (Falconer, 1989).

  $$GA = i\ h2\ \sigma_p$$

  where i is the selection intensity and σ_p the standard deviation of the phenotypic variance in F_4 population. In the present analysis 1.76 was considered for i, which is the value for 10% selection intensity.

- Correlated response:- The correlated response in PPM for selection based on DFPM was calculated as described by Falconer (1989):

  $$CR_Y = ih_X h_Y r_A \sigma_{pY}$$

  where CR_Y is the correlated response of dependent variable (Y), i selection intensity, h_X is square root of heritability of the independent variable (X), h_Y is the square root of the heritability of Y, σ_{pY} is the square root of phenotypic variance of trait Y.

Results and discussion: Table 2.6 shows that there were high phenotypic and genotypic variability for PPM. At the F_4 generation, most of the lines are homozygous for specific loci and mainly additive and additive x additive genetic variances are prevailing. High genetic variability coupled with the heritability estimates of 0.42 for PPM suggest that this trait can be manipulated reasonably well in a breeding program. The predicted genetic advance was 38 % of the population mean for PPM.

There was significant negative association between DFPM and PPM (Fig.2.1). Pearson correlation coefficient between the two traits was -0.69 ($p < 0.001$). It appears that indirect selection could be made for PPM based on DFPM in situations where evaluation for PPM is difficult. The predicted correlated response in PPM for selection in DFPM

was 29%. This is closer to what was predicted for direct selection, indicating that selection based on DFPM is effective. This analysis was based only on one population, i.e., 272-2 X CDC Anna. The other two populations 298T-9 X CDC Anna and 298T-9 X CDC Frontier had very low proportion of matured pods by the time of the first snowfall and could not effectively be rated for PPM.

Table. 2.6. Heritability and predicted genetic gain for DFPM and PPM at four months after planting in F_4 population of 272-2 X CDC Anna population, as assessed in the field in 2004

Parameter	Days to first pod maturity (DFPM)	Percent pod maturity (PPM)
Mean	99	50
Range	84 – 118	10 – 88
σ^2_P	75.1	662.5
GCV (%)	8.1	41.5
h^2	0.38	0.42
GA	5.9	37.9

σ^2_P - phenotypic variance , GCV – genetic coefficient of variation, h^2 – narrow sense heritability, GA- genetic advance expressed as percent of the population mean

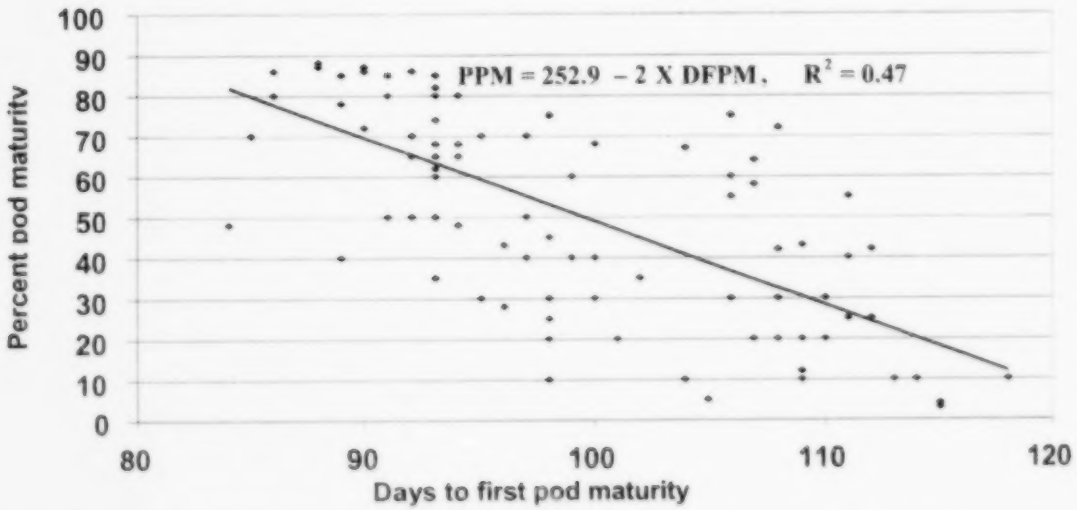


Fig. 2.1. Association of percent pod maturity (PPM) with days to first pod maturity (DFPM) in 272-2 X CDC Anna population

THEME 3: Effects of double podding, early flowering and short internode length alleles on maturity duration in chickpea

Favorable single gene inheritance has in some cases brought about great improvements in crop breeding, like the dwarfing gene in wheat and determinate type of stem termination in beans and soybeans. We hypothesized that earliness could be induced through double podding, early flowering and short internode length in chickpea. The objective of this study was to determine the individual and combined effect of double podding, early flowering, and short internode length alleles on earliness.

3.1. Double podding allele (s)

Materials and methods: This study was conducted with the 272-2 X CDC Anna population mentioned in the preceding chapter (see sections 2.1 and 2.2). Line 272-2 has small seeds (about 130 g/1000 seeds) and produces double pods in some of its reproductive nodes. CDC Anna has high yield potential and medium seed size (about 240 g/1000 seeds) with single pod per node throughout. F_2 and F_3 populations from this cross were evaluated under greenhouse conditions. Observation was recorded on number of single podded and double podded genotypes. The numbers of single and double podded nodes were counted for double podded plants. Expressivity of double podding was calculated as reported by Kumar et al. (2000):

$$\frac{\text{Number of double podded nodes}}{\text{Number of double podded nodes + Number of single podded nodes}} \times 100$$

In a second experiment, F_2-derived F_3 lines and F_3-derived F_4 lines, each obtained from greenhouse experiments shown above, were evaluated on a micro-plot basis in summer 2004 at Saskatchewan Pulse Growers farm, Saskatoon. These nurseries were arranged in an augmented randomized complete block design (ARCBD). The parental genotypes were included as replicated checks. Data were collected on podding habit (i.e., single vs double podding), days to flowering, days to first pod maturity, and percent pod maturity at four months after planting, plant height at flowering and maturity stages and grain yield.

Data analysis was carried out using SAS PROC GLM as described by Scott and Milliken (1993). Block effects were determined from the replicated check entries and the mean of the test entries were adjusted accordingly. Effect of S/s locus on maturity was determined by comparing variation between classes (ss, Ss and SS) of individuals with different locus types relative to variation within these classes. Podding habit is controlled by a single gene in chickpea, with the recessive ss conditioning double podding (Kumar et al., 2000). Based on this evidence, F_4 plants coming from double podded F_3 parent were considered as having ss allele, those from single podded F_3 parent but showing segregation for podding habit at F_4 taken as Ss, and those with only single pod at both generations as SS for the podding habit locus.

Results and discussion: Segregation for podding habit followed Mendelian inheritance as reported previously (Kumar et al. 2000). The proportion of double podded genotypes

was 24.5% in F_2 generation and 38.4% in F_3 generation in greenhouse studies, very close to the expected values for single recessive gene inheritance (Table 3.1). Expressivity of double podding ranged from 1.5 to 34.5 % in the F_2 population. In F_3 it ranged from 1.3 – 29.3%. Kumar et al (2000) also reported that expressivity of double podding in chickpea recombinant inbreed lines ranged from 2-30%.

Table 3.1. Percentage of double podded genotypes and expressivity of double podding in F_2 and F_3 populations of 272-2 X CDC Anna under greenhouse conditions

Parameter		F_2	F_3
Percentage of double podded genotypes	Observed	24.5	38.4
	Expected	25	37.5
Expressivity of double podding	Range	1.5 – 34.5	1.3 – 29.3
	Mean	8.6	14.4

Under field conditions, the 272-2 X CDC Anna population showed a wide range of variation in percent pod maturity at four months after planting (Fig. 3.1). Half of the population had less than 50% pod maturity at four months after planting. The late maturing parent CDC Anna also fell in this range, while 272-2 had an average of 67% pod maturity. Some genotypes (< 20% of the total population) exceeded both parents and attained more than 75% pod maturity at four months after planting. Some of these could be exploited as sources of earliness in chickpea breeding.

The effect of S/s locus was significant on days to first pod maturity and post flowering increase in height between flowering and maturity stages (Table 3.2). The presence of ss allele led to an earlier start of maturity of lower pods and through this and other mechanisms limited post flowering growth in height. Mean percent pod maturity was higher (by about 5%) for double podded genotypes over single podded genotypes, but was not significant statistically. This could be ascribed to the other maturity genes possibly segregating in the population which made within group variation high. The top 10% lines in percent pod maturity were generally the double podded genotypes. The greenhouse experiment on the F_2 population also showed similar results. Double podding increases the sink size and as a result of intensified competition for photoassimilate this led to minimized post-flowering growth and earlier crop maturity.

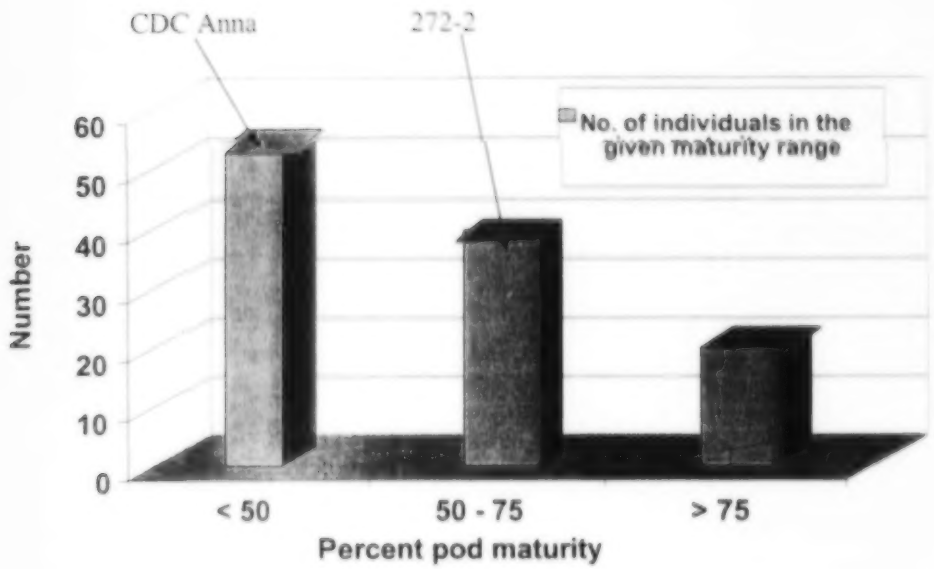


Fig.3.1. Distribution of 272-2 X CDC Anna F_4 chickpea population in percent pod maturity assessed four months after planting at SPG, Saskatoon in summer 2004

Table 3.2. Least square means of the three SS genotypes for different earliness traits and grain yield in 272-2 X CDC Anna cross grown at SPG in 2004

Genotype	DFPM	PPM	IH	Grain yield (g/plot)
SS – single podded	101 a	49.2 a	24.3 a	139.2 a
Ss – segregating	100 ab	45.0 a	22.1 ab	129.6 a
Ss – double podded	97 b	53.9 a	21.3 b	136.1 a
$a(SS)^1$	2	-	1.5	-
$d(SS)^2$	1	-	0.7	-

DFPM – days to first pod maturity, PPM – percent pod maturity, IH- increase in height between flowering and maturity times, means followed by different letters in a column are statistically significant at $P \leq 0.05$.

$a(SS)^1$- additive effect of SS gene calculated as the mid-point of the difference between the early and late mean values, $d(SS)^2$ – dominance effect of SS gene calculated as the deviation of the heterozygote from the homozygote mean values.

3.2 Major early flowering allele (efl) and polygenes effect

Materials and methods: Two populations from 298T-9 X CDC Anna and 298T-9 X CDC Frontier crosses were used to determine the effects of early flowering genes on

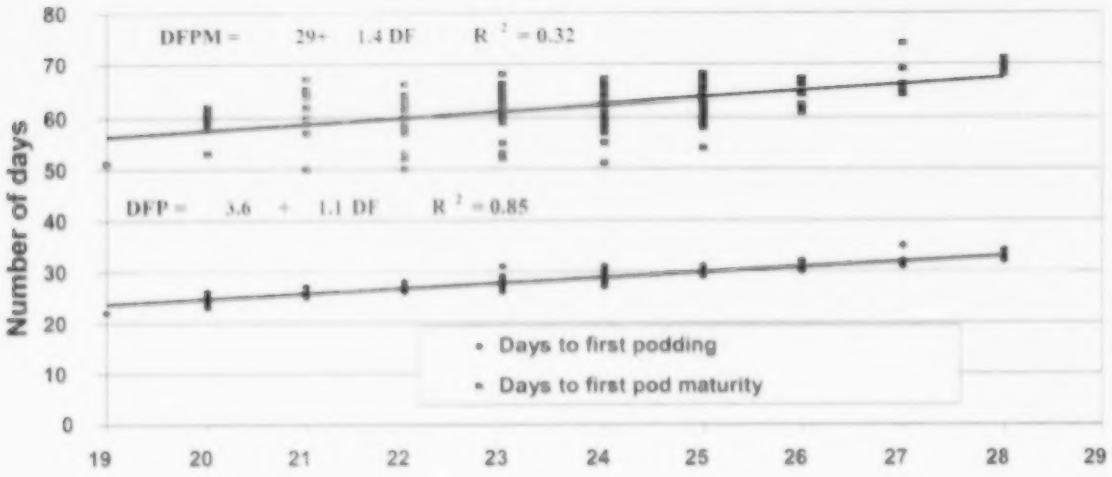
days to first pod maturity and percent pod maturity. Genotype 298T-9 is an early flowering line, whereas CDC Anna and CDC Frontier are medium to late flowering cultivars under Saskatchewan conditions. These populations were evaluated in experiments in the greenhouse in F_2 and F_3 and field in F_3 and F_4 generations (see section 2.1 and 2.2 for details of the evaluation methodology). Data were collected on days to flowering, days to first podding, days to first pod maturity and percent pod maturity at four months after planting.

Results and discussion: Greenhouse studies on F_2 populations revealed that days to first pod maturity was linearly and significantly associated with days to flowering (Fig. 3.2). Regression analysis showed that days to flowering determine 32% of the variation in days to first pod maturity in both populations. Selection of the top 5% early flowering lines were 3-6 days earlier in days to first pod maturity over the population mean across greenhouse and field experiments (Table 3.3). It appears that incorporation of early flowering alleles leads to earlier commencement of maturity of lower pods, which hastens overall progress towards maturity. Two major genes were mainly responsible for variation in time to flowering (see section 2.1). Thus, breeders can easily incorporate early flowering genes into breeding lines which will help to reduce maturity duration in chickpea.

Table 3.3. Response in days to first pod maturity for 5% selection on the basis of time to flowering in chickpea

Cross	Parameter	Greenhouse (F_2 population)	Field (F_4 population)
	N	180	115
298T-9 X CDC Anna	Mean (X)	111	62
	5% early flowering lines	106	59
298T-9 X CDC Frontier	Mean (X)	116	63
	5% early flowering lines	111	57

A) 298T-9 X CDC Anna



B) 298T-9 X CDC Frontier

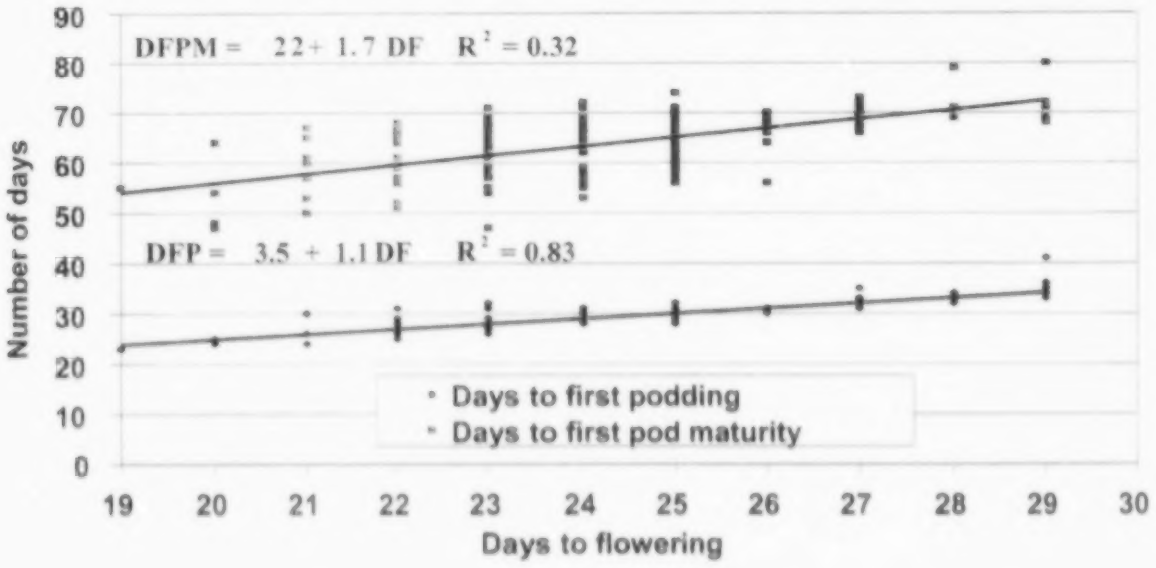


Fig. 3.2. Associations of days to flowering with days to first podding and days to first pod maturity in two populations of chickpea assessed under greenhouse conditions.

3.3. Short internode length

Materials and methods: A cross was made between the dwarf mutant-short internode accession E100Ym and the normal internode length genotype CDC Anna for this study. The average internode length for CDC Anna is 2.0 cm while it is 1.0 cm for E100Ym. The F_1 generation was advanced to F_2, and F_2 - F_4 populations were evaluated in the greenhouse and field for earliness. Assessments were taken on internode length, days to first pod maturity and percent pod maturity at four months after planting.

Results: All of the F_1 plants had normal internode length, indicating that the short internode length trait is recessive. The F_2 population segregated following the Mendelian ratio of 3 normal: 1 short internode dwarf (Table 3.4). Sandhu et al. (1990) described the dwarf phenotype in E100Ym as a single gene macro-mutation. The short internode plants were generally late to flower, pod and mature. Despite this fact, there were some differences in days to first pod maturity and percent pod maturity within the non-dwarf genotypes. This could be due to other untargeted maturity genes for which the population was segregating. But the specific allele we tried to introduce from the dwarf parent had unfavorable effects on overall plant growth and development. Yet, this does not nullify the hypothesis that short internode length could lead to early crop maturity as a different allele for this trait may still have the expected effect.

Table 3.4. Segregation for internode length/plant height in CDC Anna X E100Ym F_2 population of chickpea evaluated in greenhouse in summer 2003

Segregation	No. of F_2 plants
Normal	137
Dwarf	43
Total	180
χ^2	0.07
P value	0.7 – 0.8

3.4. Comparison of the effects of short internode length, double podding and early flowering traits on earliness and other agronomic traits and yield

Materials and methods: From the $F_{3:4}$ populations grown in the field in summer 2004 as shown above (see section 3.1), the three best lines were selected from each cross for further comparison. The selection was based on earliness to flower for the two early flowering populations, and expressivity of double podding for the double podding population. However, the short internode segregants from the respective cross were too late to mature and were left out at F_2. Instead the three earliest maturing lines were considered from this cross. The selections ($F_{3:5}$ generation) were grown further in greenhouse for seed multiplication and at the same time advance to $F_{3:6}$ generation. During the summer 2005 all the twelve selected lines (3 lines x 4 crosses) were grown along with the four parental lines (272-2, 298T-9, CDC Anna and CDC Frontier) and two

early check varieties (CDC Cabri and Myles) at Goodale, Saskatoon. These were arranged in a randomized complete block design with three replications. Three row plots of 4 m long with 30 cm spacing between rows was used for this experiment. The crop was protected against ascochyta blight by spraying three times with commercial fungicides recommended for chickpea. Data on days to first pod maturity, percent pod maturity, height at flowering, and plant height were recorded. DM (days from planting to when 90% of the pods turned brown) was also determined. Seed yield (kg/ha) and 100 seed weight (g) were determined after cleaning the harvested samples. Analysis of variance was carried out using SAS PROC GLM (SAS Institute Inc., 1999). Means were separated using least significant differences (LSD).

Results and Discussion: Highly significant differences were observed among the lines in phenological and other agronomic characters (Table 3.5). The three genotypes from the double podding cross were on average ten days earlier than the parents and standard checks in days to maturity. However, the 2005 season was generally cool and wet and all the genotypes took long to mature. Percent pod maturity at four months after planting was very low (< 50%) for some genotypes, whereas the double podding lines attained over 80% pods mature at this time. The early flowering group especially those from the desi x desi cross were also relatively earlier in time to maturity, but had only slight advantages over parents and check varieties. The double podding lines in this experiment had relatively small increase in height between flowering and maturity (Table 3.5). The difference between plant height and height at flowering was only 10-15 cm in the double podding lines as compared to up to 40 cm increase in other lines and varieties. The double podding lines were high yielder than most of the parents and check varieties (Table 3.5). These also had relatively higher percentage of good seeds.

Table 3.5. Mean seed yield and some phenological and agronomic characters in chickpea lines ($F_{3:6}$ generation) derived from crosses with short internode length, double podding and early flowering parents as compared to their parents and other check varieties.

Category	Entry	Percent pod maturity	Days to maturity	Height at flowering (cm)	Plant height (cm)	Seed yield (kg/ha)	100 seed weight (g)
Short internode	Y3842-005	55	146	40	68	3387 (82)	19.6
length (E100Ym x	Y3842-023	43	149	38	68	2729 (69)	15.2
CDC Anna)	Y3861-041	71	139	40	60	3117 (83)	19.5
Double podding	Y9421-026	88	129	38	52	3020 (78)	16.8
(272-2 x CDC Anna)	Y9463-028	83	132	42	51	2896 (76)	13.2
	Y4912-039	83	134	39	56	2773 (78)	15.1
Early flowering	Y6161-009	77	138	40	54	3722 (85)	18.2
(298T-9 x CDC	Y6172-011	71	142	39	57	3435 (83)	17.8
Anna)	Y1611-040	53	149	39	70	2340 (72)	15.6
Early flowering	Y7211-039	52	148	39	61	2015 (66)	21.8
(298T-9 x CDC	Y2721-065	43	147	37	67	2491 (78)	20.8
Frontier)	Y2721-089	58	145	36	65	2779 (66)	20.2
Parental genotypes	272-2	76	142	34	54	2706 (74)	13.4

	298T-9	36	149	37	65	2256 (66)	18.6
	CDC Anna	25	153	41	80	1364 (64)	19.9
	CDC Frontier	35	151	46	62	2342 (55)	35.9
Check varieties	CDC Cabri	57	145	45	69	3277 (82)	29.2
	Myles	63	145	41	69	2132 (76)	18.8
CV (%)		11.4	3.6	8.4	12.1	16.2	3.8
$LSD_{0.05}$		21.2	9.2	5.5	12.6	1156	4.4

Note: In seed yield column, the figures in parenthesis show the percentage of healthy, mature seeds.

3.5. Gene pyramiding for earliness in chickpea

Materials and methods: Intercrosses were made among double podding (272-2), early flowering (298T-9) and short internode length (E100Ym) parents to pyramid the genes for these traits and assess their combined effect on earliness. The pedigree for this cross was 272-2/E100Ym//298T-9/E100Ym. The F_2 population consisting of 180 individuals was evaluated in the greenhouse during summer/fall 2004 along with 272-2 and CDC Anna as repeated checks. Individual plants were grown in 20 cm pots. From these, 128 $F_{2:3}$ genotypes for which sufficient seed was available were grown at Preston, Saskatoon in summer 2005. Each genotype was planted in a three row micro-plot of about 1 m long. The experiment was laid out in augmented randomized complete block design using 272-2, 298T-9, CDC Anna and CDC Cabri as replicated checks. In both greenhouse and field experiments data on days to flowering, pod number per node, internode length, height at flowering, plant height, days to first pod maturity, percent pod maturity at four months after planting, days to maturity (for field experiment only), number of pods per plant, 100 seed weight, and grain yield were collected.

SAS PROC UNIVARIATE analysis was used to assess variability within the segregating population. Pearson correlation coefficients among the phenological and agronomic traits were determined for the field grown $F_{2:3}$ population. The direct and indirect effects of days to flowering on days to maturity were determined using a path coefficient analysis (Bowley, 1999).

Results and discussion: Wide variability among F_2 individuals was detected for the different earliness traits considered. Days to first pod maturity ranged from 57 to 80 days, with some genotypes earlier than the best parental check 272-2 by up to one week (Table 3.6). The variability in percent pod maturity at four months after planting was correspondingly high, ranging from 46-100% (Table 3.6). A few genotypes had over 90% pod maturity at this time, which means that these had reached full maturity in four months. However, the same level of earliness may not be attained under field conditions, especially in wet seasons. These early genotypes were superior to 272-2 and CDC Anna which had mean percent pod maturity of 84% and 74%, respectively. This study shows that some progress has been made in identifying chickpea germplasm earlier maturing than currently available cultivars.

Table 3.6. Mean, range, and standard deviation of some agronomic and phenological traits in an F_2 chickpea population from a multiple cross, along with checks (272-2 and CDC Anna) in a greenhouse experiment in 2004

Parameter	Mean	Range	272-2	CDC Anna
Days to flowering	27	23-34	25 ± 0.7	29 ± 0.5
Days to first pod maturity	70	57-80	64 ± 4.1	74 ± 2.5
Percent pod maturity	71	46-100	84 ± 18.7	74 ± 14
Internode length (cm)	2.0	1.2-2.7	2.1 ± 0.3	2.1 ± 0.3
Plant height (cm)	59.1	43-82	57.6 ± 9.6	65.5 ± 6.4
No. of pods/plant	106.4	29-171	130.9 ± 19.8	78.9 ± 13.1
Grain yield (g/plant)	37.3	11.8-51.8	26.2 ± 11.1	39.2 ± 4.1

Table 3.6. Pearson correlation coefficients among some phenological and agronomic traits in $F_{2:3}$ population of chickpea (N = 126) from intercrosses among short internode length, double podding and early flowering parents and evaluated at Preston, Saskatoon in 2005.

Character	DFPM	PPM	DM	PTHT	100 SW
Days to flowering (DF)	0.46**	-0.50**	0.44**	0.43**	0.24**
Days to first pod maturity (DFPM)	-	-0.78**	0.73**	0.35**	0.26**
Percent pod maturity (PPM)		-	-0.82**	-0.36**	-0.18*
Days to maturity (DM)			-	0.38**	0.22*
Plant height (PTHT)(cm)				-	0.36**
100 seed weight (100 SW) (g)					-

*, ** - significant at $P \leq 0.05$ and $P \leq 0.01$, respectively.

Table 3.7. Partial path analysis for the direct and indirect effects of days to flowering on days to maturity in $F_{2:3}$ population of chickpea (N = 126) from intercrosses among short internode length, double podding and early flowering parents and evaluated at Preston, Saskatoon in 2005.

Type of effect	Coefficient
Direct effect	0.10
Indirect effect via days to first pod maturity	0.30
Indirect effect via plant height (cm)	0.05
Indirect effect via 100 seed weight (g)	- 0.01
Total (= r)	0.44
R^2	0.58

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C) Papers/Presentations

The results of this work were presented at the following meetings.

Oral presentations

Yadeta Anbessa, Tom Warkentin, Rosalind Ball and Bert Vandenberg. 2005. Genetics and early maturity strategies in chickpea. Proceedings of the North American Pulse Improvement Association. Oct 28-29, Newark,Delaware.

Yadeta Anbessa, Tom Warkentin, Rosalind Ball and Bert Vandenberg. 2004. Gene pyramiding for earliness in chickpea. Proceedings of the 5th Canadian Pulse Research Workshop, Nov. 28-30, 2004, London, Ontario.

Poster presentations

1. Yadeta Anbessa, Tom Warkentin, Bert Vandenberg and Rosalid Ball. 2005. Two major genes plus polygenes for time to flowering in chickpea. 4th International Food Legumes Conference, October 18-22, 2005, New Delhi, India.

2.Yadeta Anbessa, Tom Warkentin, Rosalind Ball and Bert Vandenberg. 2005. Early maturity strategies in chickpea: pyramiding key genetic traits.
-Pulse Days 2005, Saskatchewan Pulse Growers, Saskatoon, Canada
-Soils and Crops 2005, Extension Division, University of Saskatchewan, Saskatoon, Canada

3.Yadeta Anbessa, Tom Warkentin, Rosalind Ball, and Bert Vandenberg. 2003. Inducing earliness in chickpea through secondary traits.
-North American Pulse Improvement Association, October 2003, Sacramento, USA
-Pulse Days 2004, Saskatchewan Pulse Growers, Saskatoon, Canada

-Soils and Crops 2004, Extension Division, University of Saskatchewan, Saskatoon, Canada

4.Yadeta Anbessa, Tom Warkentin, Bert Vandenberg, and Rosalind Ball. 2003. Early flowering and short internode length as components of early maturity in chickpea.
-Pulse Days 2003, Saskatchewan Pulse Growers, Saskatoon, Canada
-Soils and Crops 2003, Extension Division, University of Saskatchewan, Saskatoon,
Canada

Manuscripts

1. Yadeta Anbessa and Tom Warkentin. 2005. On improving crossing success in chickpea. Plant Breeding 124: 608-609.
2. Yadeta Anbessa, Tom Warkentin, Bert Vandenberg and Rosalind Ball.2006. Inheritance of time to flowering in chickpea in a short season temperate environment. J. of Heredity (accepted).
3. Yadeta Anbessa, Tom Warkentin, Bert Vandenberg and Manjula Bandara. 2006. Heritability and predicted gain from selection in components of crop duration in divergent chickpea cross populations. Euphytica (submitted).
4. Yadeta Anbessa, Tom Warkentin, Bert Vandenberg and Rosalind Ball and Yantai Gan. 2006. Relationships of dry matter accumulation and partitioning with timing of crop maturity in chickpea (in preparation).
5. Yadeta Anbessa, Tom Warkentin, Bert Vandenberg and Rosalind Ball. 2006. Effects of short internode length, double podding, and early flowering on earliness and other agronomic traits and yield of chickpea (in preparation)

D) Information of benefit to producers, processors, or governments

Early maturing genotypes were found to partition a higher proportion of dry matter to pods early in the season than did late ones. This shows that preferential partitioning of dry matter to pods is partly responsible for earliness of crop maturity in chickpea in western Canada. This strategy also maximizes yield especially when the end of the season is delimited by drought or frost.

Some lines that seem to be earlier than the best parents and presumably superior to available cultivars in terms of earliness have been identified. It was observed that double podding and early flowering traits contributed to superiority of these lines in earliness. Genetic studies revealed that days to flowering is controlled by two major genes along with other polygenes in chickpea, with epistatic interaction between the two major genes. The heritability estimate of this trait was high (> 80%) across different populations. On the other hand, days to first pod maturity and percent pod maturity had moderate heritability estimates. This information is useful to design effective selection strategies for improvement of chickpea with respect to earliness and yield.

E) Personnel

Mr. Yadeta Anbessa conducted this research as the major portion of his PhD thesis research project in the Department of Plant Sciences, University of Saskatchewan. Mr. Anbessa began his PhD in September 2002. He expects to defend his thesis in early 2006.

F) Equipment

No equipment was purchased in this project.

G) Project developed materials

Segregating F_5 populations have been developed. Some of these lines will enter the CDC breeding program for multi-location testing in 2006 and potential release as varieties in the future. Some lines from this research are being used as sources of earliness in the CDC crossing program.

H) Project photos

Mr. Anbessa has taken photos of some early maturing genotypes and their parents. These are available on request.

I) Acknowledgement

The Saskatchewan Agricultural Development Fund was acknowledged in all presentations, publications and manuscripts where this research project was mentioned.

J) Expense statement

Will be supplied.

K) ICAR Data Entry

This project has been entered into ICAR.